

281642US0XPCT.ST25
SEQUENCE LISTING

<110> Patek, Miroslav
Elisakova, Veronika

<120> FEEDBACK RESISTANT ACETOHYDROXY ACID SYNTHETASE MUTANTS

<130> 281642US0XPCT

<140> US 10/561,906

<141> 2005-12-21

<150> PCT/EP04/06157

<151> 2004-06-08

<150> EP 03014640.1

<151> 2003-06-26

<160> 12

<170> PatentIn version 3.3

<210> 1

<211> 519

<212> DNA

<213> Artificial Sequence

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<223> Synthetic DNA

<220>

<221> CDS

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gac gta gac gat gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc	96
Asp Val Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg	
20 25 30	
gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc	144
Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly	
35 40 45	
atc aac cgc atc acg gtt gtt gtc gac gcc gac gag ctc aac att gag	192
Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu	
50 55 60	
cag atc aac aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg	240
Gln Ile Asn Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val	
65 70 75 80	
cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag	288
Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys	
85 90 95	
gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac	336
Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn	
100 105 110	
atc ttc cgc gcc cga gtc gtc gac gtg gct cca gac tct gtg gtt att	384
Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile	
115 120 125	

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gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtg atg	432
Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met	
130 135 140	
gaa caa ttc gaa atc cgc gaa ctg atc caa tcc gga cag att gca ctc	480
Glu Gln Phe Glu Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu	
145 150 155 160	
aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa	519
Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile	
165 170	

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Met Val Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
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Asp Val Asp Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 20 25 30

Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
 35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
 50 55 60

Gln Ile Asn Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
 65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
 85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
 100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
 115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
 130 135 140

Glu Gln Phe Glu Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
 145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
 165 170

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<211> 519
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<400> 3
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 Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
 1 5 10 15
 gac gta gac ggt gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc 96
 Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 20 25 30
 gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc 144
 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
 35 40 45
 atc aac cgc atc acg gtt gtt gtc gac gcc gac gag ctc aac att gag 192
 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
 50 55 60
 cag atc acc aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg 240
 Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
 65 70 75 80
 cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag 288
 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
 85 90 95
 gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac 336
 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
 100 105 110
 atc ttc cgc gcc cga gtc gtc gac gtg gct cca gac tct gtg gtt att 384
 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
 115 120 125
 gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtg atg 432
 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
 130 135 140
 gaa cca tcc gga atc gcg gaa ctg atc caa tcc gga cag att gca ctc 480
 Glu Pro Ser Gly Ile Ala Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
 145 150 155 160
 aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa 519
 Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
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<210> 4
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 <212> PRT
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<400> 4

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Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
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Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
20 25 30

Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
50 55 60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
130 135 140

Glu Pro Ser Gly Ile Ala Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
165 170

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<400> 5
gcggaggaag tactgcc

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<400> 6
caatcagatt aattgctgtt ta

22

<210> 7
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<400> 7
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<400> 8
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Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
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Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 20 25 30

Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
 35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp
 50 55

<210> 11
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 <212> PRT
 <213> S. cinamonensis

<400> 11

Met Ser Thr Lys His Thr Leu Ser Val Leu Val Glu Asn Lys Pro Gly
 1 5 10 15

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Val Leu Ala Arg Ile Thr Ala Leu Phe Ser Arg Arg Gly Phe Asn Ile
20 25 30

Asp Ser Leu Ala Val Gly Val Thr Glu His Pro Asp Ile Ser Arg Ile
35 40 45

Thr Ile Val Val Asn
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<212> PRT
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Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg
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Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
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Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
35 40 45

Lys Ser His Ile Trp Leu Leu Val Asn
50 55